

IN THE SPECIFICATION:

Page 18, please replace the paragraph beginning on line 6 with the following rewritten paragraph:

Stratagene provided a genomic Hyacinth Macaw Lambda FixII Library (Cat. No. 946402). Plaques were screened at moderate stringency with a 1.3Kb Chicken *CHD-W* subclone (spans 2670-4003 nucleotides in the related Mouse *CHD1* gene (Delmas *et al.*, 1993)). A *CHD-W* genomic fragment was isolated and aligned to the chicken and mouse homologues to allow the design and construction of 3 primers (5' to 3')

P3 AGATATTCCGGATCTGATAGTGA (SEQ ID NO: 38),

P2 TCTGCATCGCTAAATCCTTT (SEQ ID NO: 39) and

P1ATATTCTGGATCTGATAGTGA(C/T)TC (SEQ ID NO: 37).

Page 19, please replace the paragraph beginning on line 20 with the following rewritten paragraph:

All the birds listed above were sexed from DNA using exactly the same PCR reaction. PCR reaction volumes of 20 μ l were made up of Promega Taq buffer (1x is 50mM KCl, 10mM Tris.HCl, 1.5 mM MgCl₂, 0.1% Triton X-100), 200 μ M of each dNTP, P2 (5'-TCTGCATCGCTAAATCCTTT) (SEQ ID NO: 39) and P3 (5'-AGATATTCCGGATCTGATAGTGA) (SEQ ID NO: 38) primers (approx 1 μ M), 50-200 ng of genomic DNA and 0.15 units of Taq polymerase. The thermal treatment was 94 °C/1.5 mins followed by 30 cycles of 55 or 56 °C/15 sec, 72 °C/15 sec, and 94 °C/30 sec with a finish of 56 °C/1 min and 72 °C/5 min. *HaeIII* (5 units; Promega) was used to cut 8 μ l of PCR product in 1x Promega restriction enzyme buffer 3 and 50 ng/ μ l bovine serum albumin (Sigma) in a total volume of 10 μ l. The digests and uncut PCR product were precipitated before being electrophoresed in a visigel (Stratagene) with ethidium bromide (40 ng/ml) at 3.5 V/cm.

Page 29, please replace the paragraph beginning on line 21 with the following rewritten paragraph:

The *HaeIII* restriction enzyme cut the *CHD-1A* fragment alone in all 3 \pm 3 species (Fig 17) and, from the sequence data, would also have worked on the Spix's Macaw (Fig 16). Figure 17 shows that the *CHD-1A* in males is cut into two fragments (45bp, 59bp) which are not easily visible on the gel. In females *CHD-W* is uncut by *HaeIII* so remains at 104bp. The discrimination using *HaeIII* provided correct sex identification in all individuals.

Page 32, please replace the paragraph beginning on line 22 with the following rewritten paragraph:

The second functional domain was identified by Delmas *et al.* (1993) as having sequence selective DNA binding capacity. Whether this is highly specific or just A+T rich regions was not established. They also noted that this domain contains Lys-Arg-Pro-Lys-Lys (SEQ ID NO: 40) and Arg-Gly-Arg-Pro-Arg (SEQ ID NO: 41) motifs which enable genes like *HMG-1*, *DI* and *Engrailed* to bind in the minor groove of A+T rich DNA.